

AMENDMENTS TO THE SPECIFICATION

Please replace paragraph [0037] with the following paragraph:¹

Nucleic acid sequences and corresponding amino acid sequences coding an R1 protein are described from different species such as potato (WO 97 11188, GenBank Acc.: AY027522, Y09533), wheat (WO 00 77229, U.S. Pat. No. 6,462,256, GenBank Acc.: MN93923, GenBank Acc.: AR236165), rice (GenBank Acc.: MR61445, GenBank Acc.: AR400814), maize (GenBank Acc.: MR61444, GenBank Acc.: AR400813), soybean (GenBank Acc.: MR61446, GenBank Acc.: AR400815), citrus (GenBank Acc.: AY094062) and Arabidopsis (GenBank Acc.: AF312027). The identified nucleic acid sequences and amino acid sequences coding R1 proteins are published by NCBI (See NCBI website <http://www.ncbi.nlm.nih.gov/entrez/>), among others, and are explicitly included in the description of the present application by mention of the references.

Please replace paragraph [0098] with the following paragraph:

With the help of the sequence information of nucleic acid molecules according to the invention or with the help of a nucleic acid molecule according to the invention, it is now possible for the person skilled in the art to isolate homologous sequences from other plant species, preferably from starch-storing plants, preferably from plant species of the genus *Oryza*, in particular *Oryza saliva* or from *Arabidopsis thaliana*. This can be carried out, for example, with the help of conventional methods such as the examination of cDNA or genomic libraries with suitable hybridisation samples. The person skilled in the art knows that homologous sequences can also be isolated with the help of (degenerated) oligonucleotides and the use of PCR-based methods. The examination of databases, such as are made available, for example, by the EMBL website (<http://www.ebi.ac.uk/Tools/index.htm>) or NCBI (National Center for Biotechnology Information, <http://www.ncbi.nlm.nih.gov/> website), can also be used for identifying homologous sequences, which code for OK1 proteins. In this case, one or more sequences are specified as a so-called query. This query sequence is then compared by means of statistical computer programs with sequences, which are contained in the selected databases. Such database queries (e.g. blast or fasta searches) are known to the person skilled in the art and can be carried out by various providers. If such a database query is carried out, e.g. at the NCBI (National Center for Biotechnology Information, <http://www.ncbi.nlm.nih.gov/> website), then the standard settings, which are specified

¹ All paragraph numbers cited herein refer to the paragraph numbers set forth in US 2007/0163003 ("the '003 publication"), the publication of the instant application.

for the particular comparison inquiry, should be used. For protein sequence comparisons (blastp), these are the following settings: Limit entrez=not activated; Filter=low complexity activated; Expect value=10; word size=3; Matrix=BLOSUM62; Gap costs: Existence=11, Extension=1.

Please replace paragraph [0323] with the following paragraph.

Proteins identified in accordance with Step a) are digested with trypsin, and the peptides obtained are analysed by means of MALDI-TOF to determine the masses of the peptides obtained. Trypsin is a sequence-specific protease, i.e. trypsin only splits proteins at a specified position when the proteins concerned contain certain amino acid sequences. Trypsin always splits peptide bonds when the amino acids arginine and lysine follow one another starting from the N-terminus. In this way, it is possible to theoretically determine all peptides that would be produced following the trypsin digestion of an amino acid sequence. From the knowledge of the amino acids coding the theoretically determined peptides, the masses of the peptides, which are obtained after theoretical trypsin digestion, can also be determined. Databases (e.g. Protein Prospector and Swissprot websites ~~NCBI~~ ~~http://prospector.ucsf.edu/ucsfhtml4.0/msfit.htm;~~ ~~Swissprot~~ ~~http://cbg.inf.ethz.ch/Server/MassSearch.html~~), which contain information concerning the masses of peptides after theoretical trypsin digestion, can therefore be compared with the real masses of peptides of unknown proteins obtained with MALDI-TOF-MS. Amino acid sequences, which have the same peptide masses after theoretical and/or real trypsin digestion, are to be looked upon as being identical. The databases concerned contain both peptide masses of proteins, the function of which has already been shown, and also peptide masses of proteins, which up to now only exist hypothetically by derivation from amino acid sequences starting from nucleic acid sequences obtained in sequencing projects. The actual existence and the function of such hypothetical proteins has therefore seldom been shown and, if there is a function at all, then this is usually based only on predictions and not on an actual demonstration of the function.

Please replace paragraph [0359] with the following paragraph.

The band of the protein with a molecular weight of ca. 130 kDa identified in Step e) was excised from the gel. The protein was subsequently released from the acrylamide as described under General Methods 10 b), digested with trypsin and the peptide masses obtained determined by means of MALDI-TOF-MS. The so-called "fingerprint" obtained by MALDI-TOF-MS was compared with fingerprints of theoretically digested amino acid molecules in databases (See the Mascot-~~→~~

~~http://www.matrixscience.com/search_form_select.html;~~ ProFound, and
~~http://29.85.19.192/profound_bin/WebProFound.exe;~~ PepSea:
~~http://195.41.108.38/PepSeaIntro.html websites).~~ As such a fingerprint is very specific to a protein, it was possible to identify an amino acid molecule. With the help of the sequence of this amino acid molecule, it was possible to isolate a nucleic acid sequence from *Arabidopsis thaliana* coding an OK1 protein. The protein identified with this method was designated A.t.-OK1. Analysis of the amino acid sequence of the OK1 protein from *Arabidopsis thaliana* showed that this deviated from the sequence that was present in the database (NP 198009, NCBI). The amino acid sequence shown in SEQ ID No 2 codes the A.t.-OK1 protein. SEQ ID No 2 contains deviations when compared with the sequence in the database (Acc.: NP 198009.1, NCBI). The amino acids 519 to 523 (WRLCE) and 762 to 766 (VRARQ) contained in SEQ ID No 2 are not in the sequence, which is present in the database (ACC.: NP 198009.1). Compared with Version 2 of the database sequence (Acc.: NP 198009.2), the amino acid sequence shown in SEQ ID NO 2 also contains the additional amino acids 519 to 523 (WRLCE).

Please replace paragraph [0435] with the following paragraph.

pMCS5 (Mobitec website, ~~www.mobitec.de~~) was digested with BgIII and BamHI and relegated. The obtained plasmid was designated as pML4. The nos-terminator from *Agrobacterium tumefaciens* (Depicker et al., 1982, Journal of Molecular and Applied Genetics 1: 561-573) was amplified with the primers P9 (ACTTCTgCAGCggCCgCgATCgTTCaaACATTTggCAATAAAgTTTC) and P10 (TCTAagCTTggCgCCgCTAgCAGATCTgATCTAgTAACATAgATgACACC) (25 cycles, 30 sec 94°C., 30 sec 58°C., 30 sec 72°C.), digested with HindIII and PstI, and cloned in the plasmid pML4 excised with the same enzyme. The obtained plasmid was designated as pML4-nos. A 1986 base pair long fragment containing the promoter of the polyubiquitin gene from maize (Genbank Acc.: 94464, Christensen et al., 1992, Plant Mol. Biol. 18: 675-689) and the first intron of the same gene shortened by digestion with ClaI and religation was cloned. The obtained plasmid was designated as pML8.